Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/25 03:34:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617726.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR8617726 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617726_1.fastq.gz SRR8617726_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 25 03:34:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617726.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	31,522,574
Mapped reads	30,737,749 / 97.51%
Unmapped reads	784,825 / 2.49%
Mapped paired reads	30,737,749 / 97.51%
Mapped reads, first in pair	15,540,650 / 49.3%
Mapped reads, second in pair	15,197,099 / 48.21%
Mapped reads, both in pair	30,240,908 / 95.93%
Mapped reads, singletons	496,841 / 1.58%
Secondary alignments	0
Supplementary alignments	1,690,734 / 5.36%
Read min/max/mean length	30 / 150 / 152.72
Duplicated reads (estimated)	8,982,403 / 28.5%
Duplication rate	20.67%
Clipped reads	19,347,328 / 61.38%

2.2. ACGT Content

Number/percentage of A's	1,184,681,199 / 29.17%
Number/percentage of C's	758,752,396 / 18.68%
Number/percentage of T's	1,232,363,884 / 30.35%
Number/percentage of G's	884,950,867 / 21.79%
Number/percentage of N's	146,530 / 0%

GC Percentage	40.48%

2.3. Coverage

Mean	1.3129
Standard Deviation	15.5716

2.4. Mapping Quality

Mean Mapping Quality	52.57

2.5. Insert size

Mean	393,580.76
Standard Deviation	6,083,733.63
P25/Median/P75	211 / 266 / 331

2.6. Mismatches and indels

General error rate	1.28%
Mismatches	49,914,984
Insertions	810,659
Mapped reads with at least one insertion	2.47%
Deletions	1,678,588
Mapped reads with at least one deletion	5.23%
Homopolymer indels	45.32%

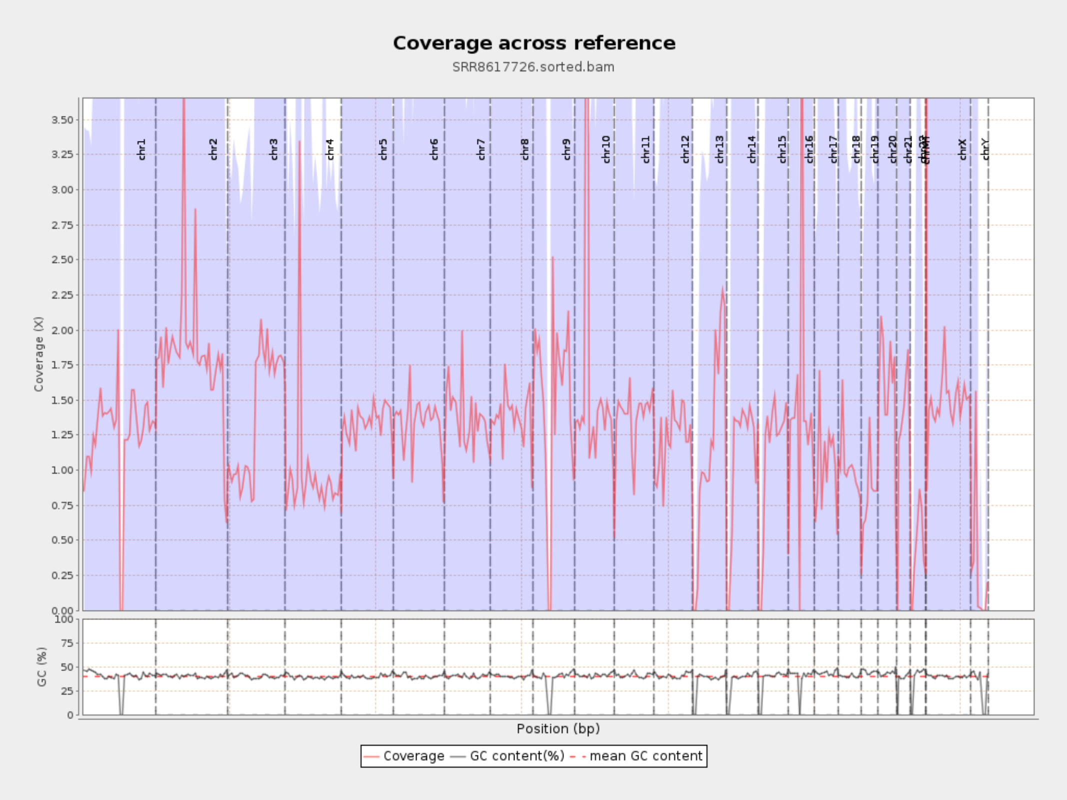
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

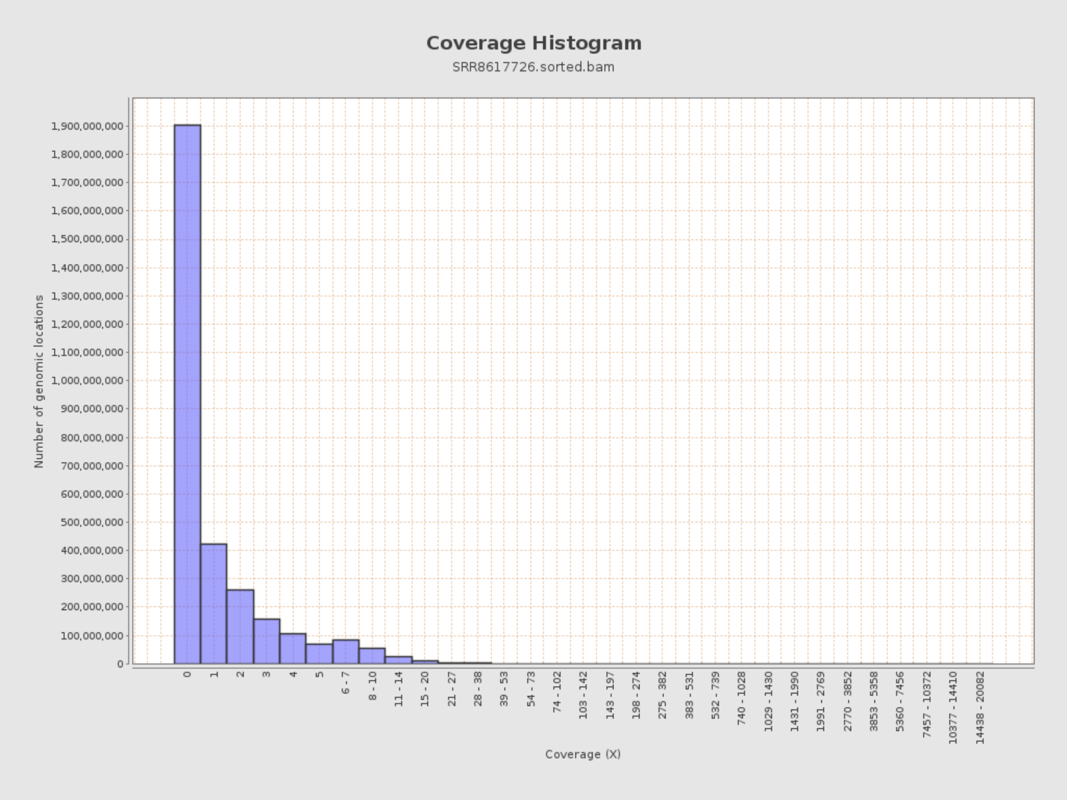
		bases	coverage	deviation
chr1	249250621	311460388	1.2496	12.2501
chr2	243199373	453888259	1.8663	18.136
chr3	198022430	275629526	1.3919	3.057
chr4	191154276	186889805	0.9777	16.3101
chr5	180915260	242507928	1.3405	2.8745
chr6	171115067	230148243	1.345	6.3778
chr7	159138663	218752138	1.3746	15.7686
chr8	146364022	202148780	1.3811	5.0386
chr9	141213431	214142011	1.5164	25.3242
chr10	135534747	220380428	1.626	43.3336
chr11	135006516	186329125	1.3801	11.6065
chr12	133851895	164077476	1.2258	7.316
chr13	115169878	137241352	1.1916	2.6044
chr14	107349540	118243144	1.1015	2.7863
chr15	102531392	111190192	1.0845	3.9359
chr16	90354753	135322894	1.4977	26.1689
chr17	81195210	85281736	1.0503	14.6852
chr18	78077248	80527028	1.0314	18.5211
chr19	59128983	49281803	0.8335	6.8428
chr20	63025520	105429103	1.6728	5.6937
chr21	48129895	62628150	1.3012	8.4827
chr22	51304566	22811494	0.4446	2.242
chrMT	16571	1349796	81.4553	40.9846
chrX	155270560	230437104	1.4841	5.7147

chrY	59373566	18160892	0.3059	24.2739

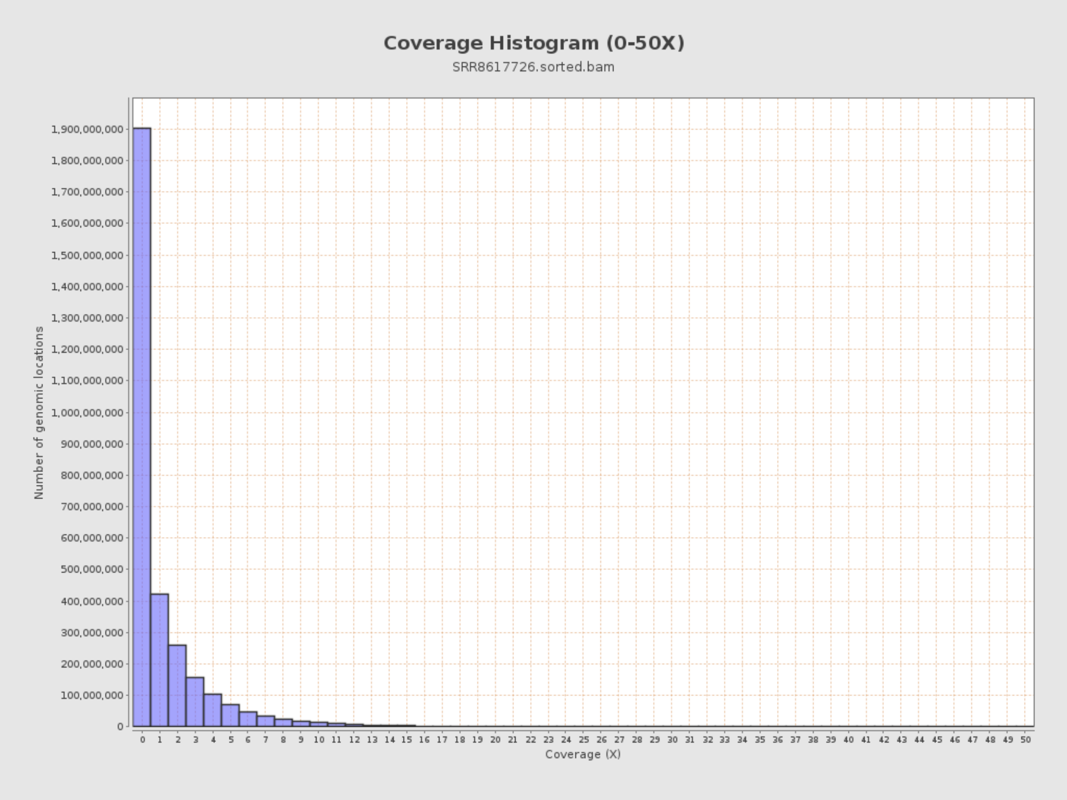
3. Results : Coverage across reference



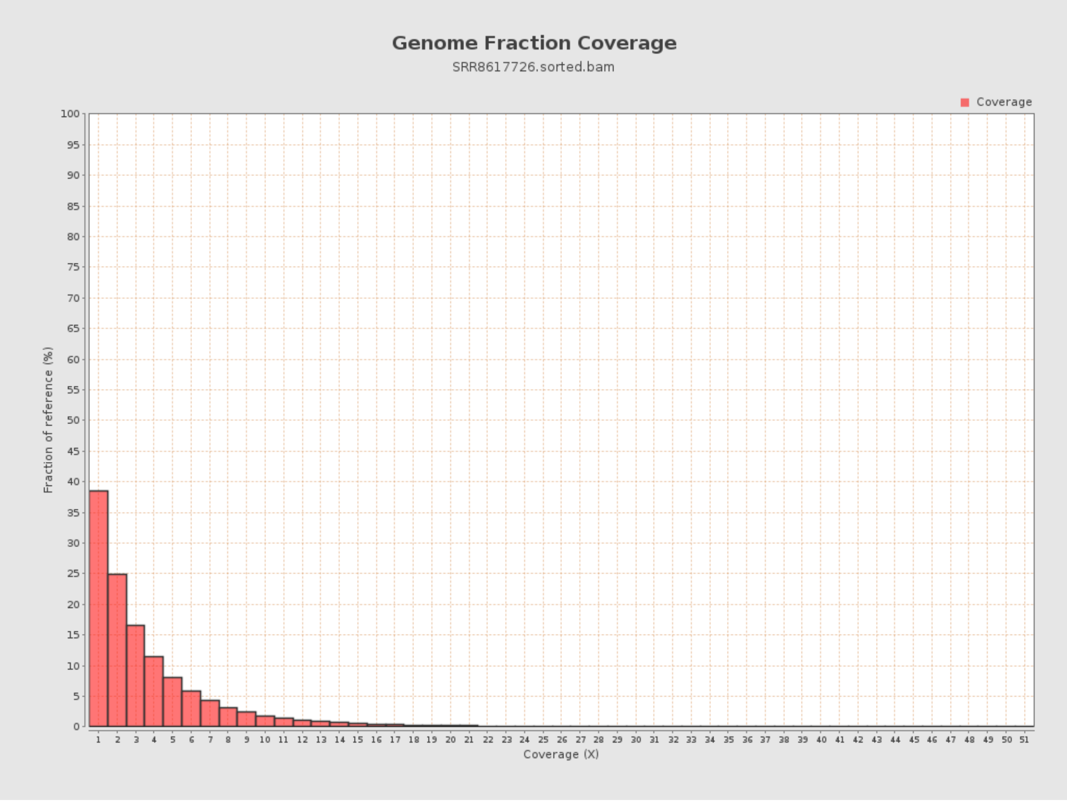
4. Results : Coverage Histogram



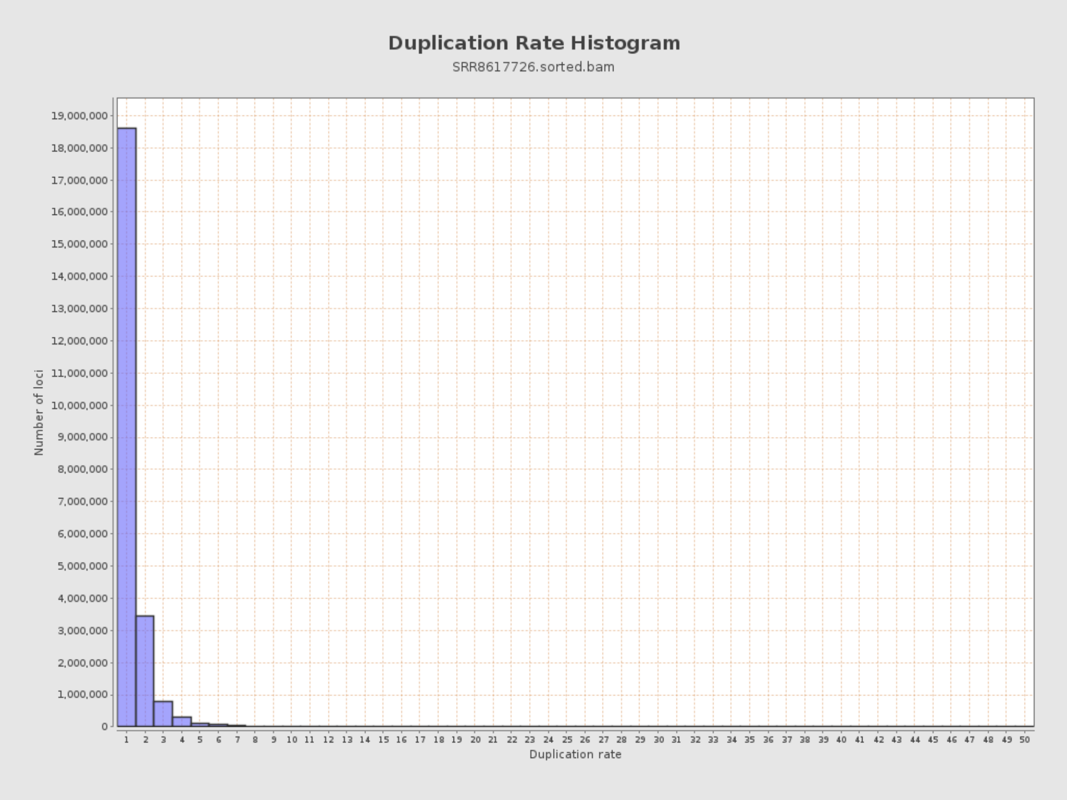
5. Results : Coverage Histogram (0-50X)



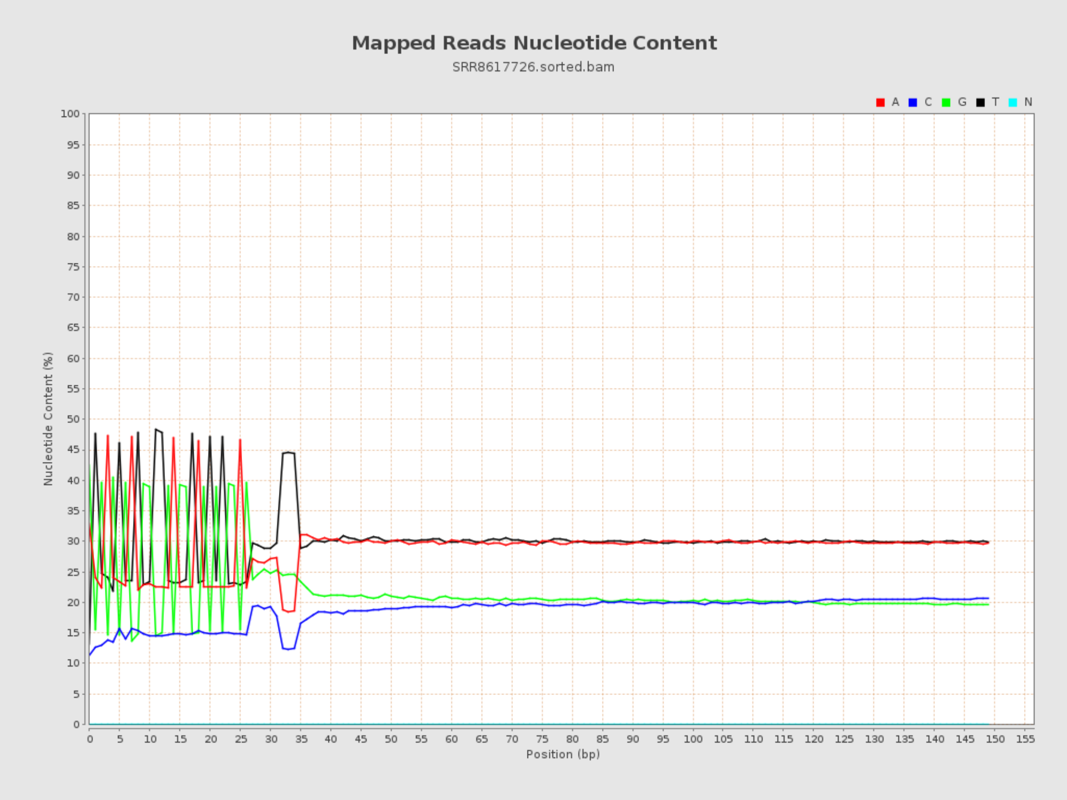
6. Results : Genome Fraction Coverage



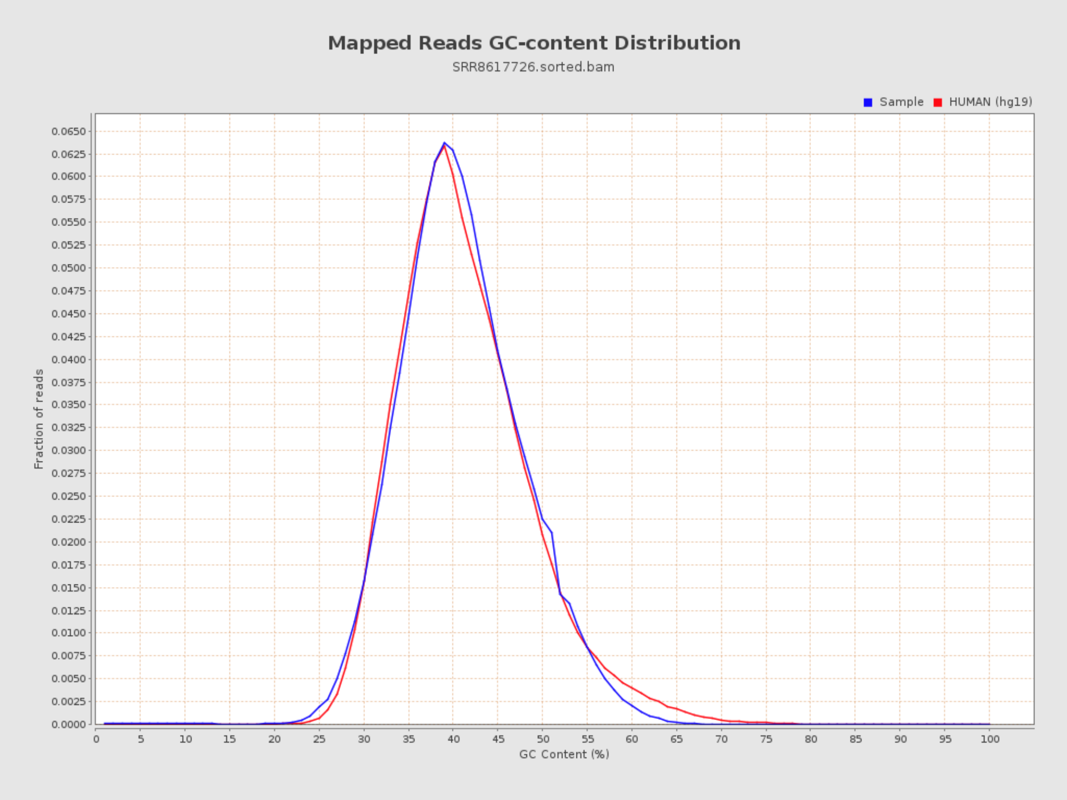
7. Results : Duplication Rate Histogram



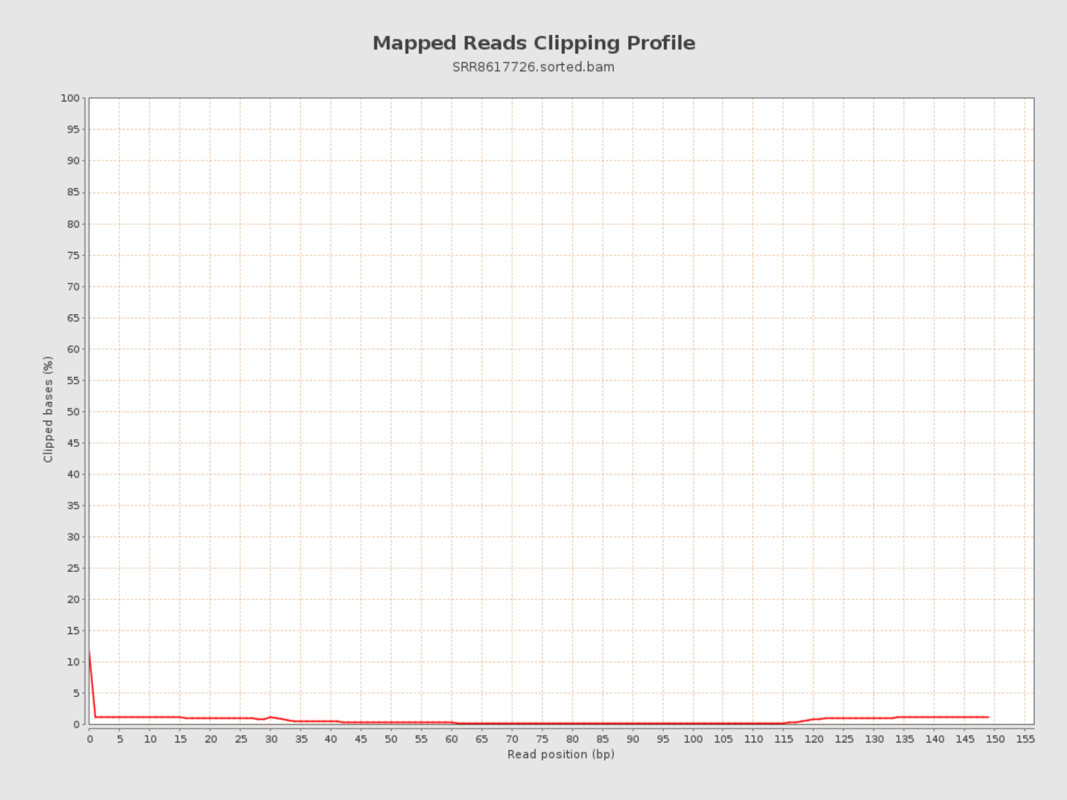
8. Results : Mapped Reads Nucleotide Content



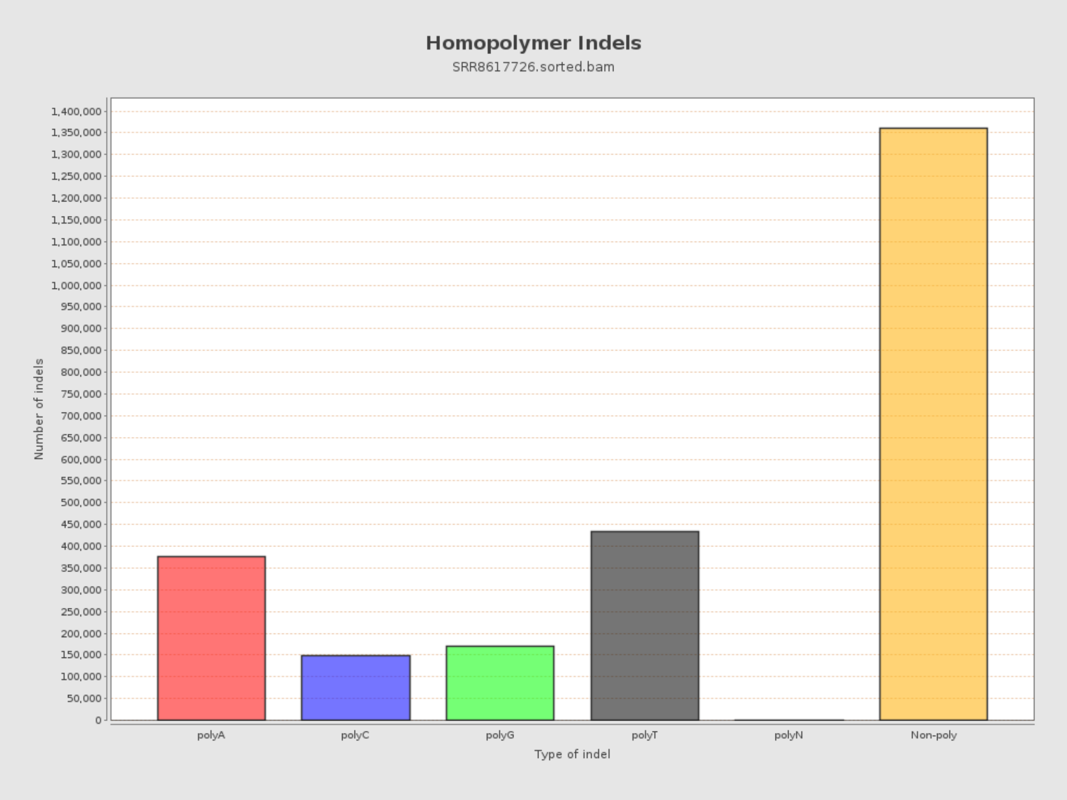
9. Results : Mapped Reads GC-content Distribution



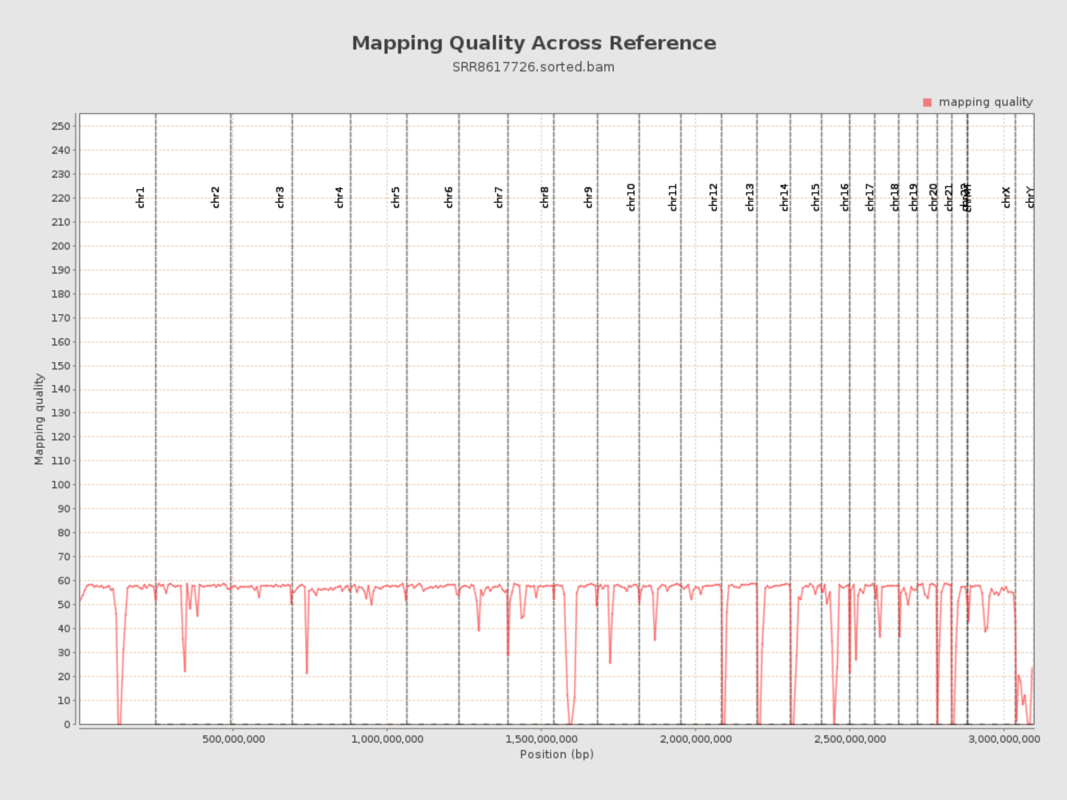
10. Results : Mapped Reads Clipping Profile



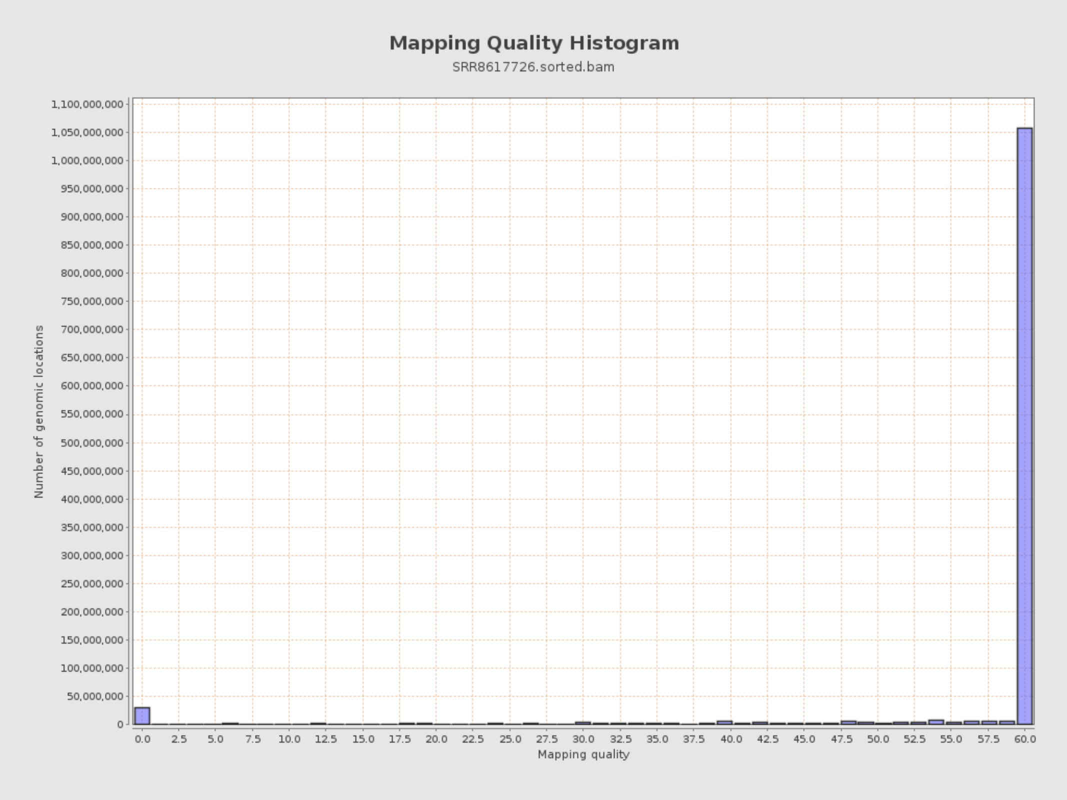
11. Results : Homopolymer Indels



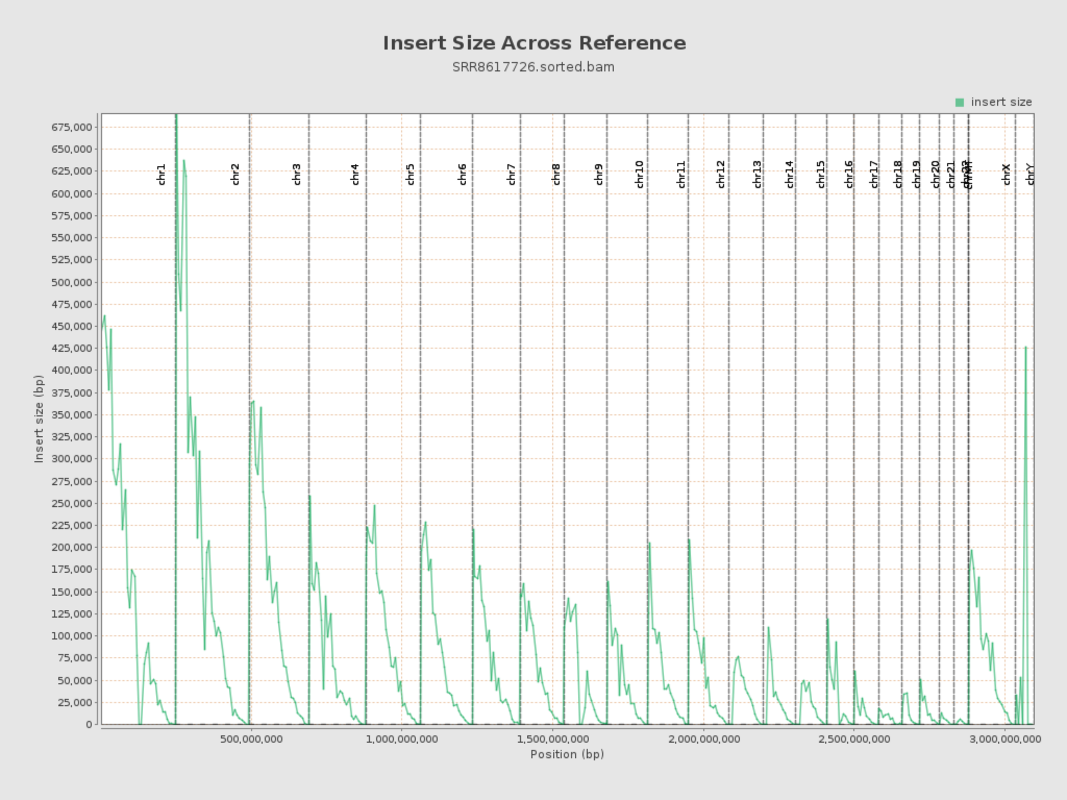
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram